Plants encounter a number of abiotic stresses, like drought, flood, salinity, high and low temperature, during their entire life cycle. These environmental stresses are the most limiting factors for agricultural production. In fact these stresses cannot be stated individually as many of their effect and responses are interlinked. The cellular machinery in response to stress includes transcription factors (activators and repressors), transcription cofactors, post transcriptional regulators, translational and post translational regulators, enzymes encoding compatible solutes, solute transporters, reactive oxygen species etc.

The classical breeding programs and even the initial attempts with genetic engineering to raise stress tolerant plants have met with limited success (Richards, 1996). This is due to lack of clear understanding of molecular basis of stress tolerance. Via recent advances in genetic and microarray analysis, some knowledge about stress perception, stress signaling (like ABA dependent and independent pathways), transcription regulators (like DREB, bZIP factors, ERFs etc.) has been gained from model organisms like *Arabidopsis, Synechosystis* and *Clamydomanas*. A detail understanding of stress response and adaptation in crop plants could be of help in raising stress tolerant cultivars and increasing crop productivity. This becomes more important for monocot crop plants like rice where due minute differences, the technologies developed in dicot model plants, may not be directly implicated (Tester and Bacic, 2005).

In order to adapt to any environment, each gene product is needed at a certain threshold that differ from gene to gene and system to system. With changing environment, this threshold changes to a new level (higher or lower than before). Hence, it becomes extremely important to
study the regulation of stress responsive genes (up- or down-regulated) 
for a complete molecular understanding of stress response in tolerant 
and sensitive cultivars. A detailed knowledge about the regulation of 
stress responsive gene will, thus, help in developing technologies that 
will mimic the cell environment of a tolerant variety of crop plant within 
the cell system of a sensitive variety, under stressed condition. A major 
regulation of various genes occurs in their promoters. This has drawn 
attention of scientists, all over the world, to study regulation of genes at 
promoter level.

During earlier studies in our lab and also reported elsewhere, a set of 
genomes that are differentially regulated in response to salinity stress have 
been identified in rice (indica varieties). Two such genes were Ribosomal 
Protein L32 (rpL32; downregulated) and multiple stress regulated MAPK2 
(MSRMK2; unregulated). The ribosomal proteins and MAPKs are 
extremely important for proper growth and development of any organism, 
a feature which is severely affected in crop plants under stress 
conditions. This study was conducted with the aim to know the 
regulatory keys (factors and phenomenons) in promoter of these two 
genomes that could be playing a major part in determining their transcript 
level under control and stress conditions. The studies on these genes can 
also give clues to the stress regulation of transcripts of other similarly 
behaving genes. Such studies are needed to find the checkpoints in 
transcriptional regulation that differentiates tolerant varieties of rice from 
the sensitive ones which in turn, will be useful in engineering and 
manipulating these switches in the sensitive varieties in order to increase 
their stress tolerance level.